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From: Kaushal, Sumesh  
Sent: Friday, April 22, 2005 11:16 AM  
To: STIC-Biotech/ChemLib  
Subject: 10735014: SEQ and interference search

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10/735014: SEQ and interference search

Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

Inventor: GODDARD, AUDREY

Please search

SEQ ID NO:83

PRT 431 aa

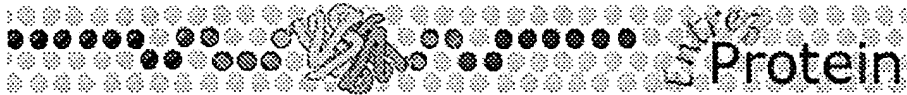
thanks

S.Kaushal

AU1636, REM2.B85

Ph: 571-27-20769

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[#9](#) Search pro361

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17:29:41 [309](#)

17:29:32 [2](#)

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Apr 18 2005 07:16:12

Search
Protein
for

Range: from
begin
to
end
Features:
☐ SNP
☐ CDS
☒ MSC
☐ HSPD
☐ STS

☒ 1: AAQ88926
Reports
FFGG316 [Homo sap...[gi:37182248]
[Blink](#), [Links](#)

LOCUS
AAQ88926
431 aa
linear
PRI 03-OCT-2003

DEFINITION
FFGG316 [Homo sapiens].
ACCESSION
AAQ88926
VERSION
AAQ88926.1
GI:37182248
DBSOURCE
accession AY358563.1
KEYWORDS
.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (residues 1 to 431)
AUTHORS
Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J., Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B., Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E., Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S., Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C., Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V., Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K., Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z., Goddard,A., Wood,W.I. and Godowski,P.
TITLE
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale Effort to Identify Novel Human Secreted and Transmembrane Proteins: A Bioinformatics Assessment
JOURNAL
Genome Res. 13 (10), 2265-2270 (2003)
PUBMED
12975309
REFERENCE
2 (residues 1 to 431)
AUTHORS
Clark,H.F.
TITLE
Direct Submission
JOURNAL
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA
COMMENT
Method: conceptual translation.
FEATURES
Location/Qualifiers
source
1..431
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/db\_xref="taxon:9606"
/clone="DNA45410"
Protein
1..431
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1..431
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/coded\_by="AY358563.1:226..1521"
/note="PRO361"
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61 edcinscst knisgdkacn lmifdtrkta rqpncylffc pneeacplkp aglmsyrii
121 tdfpsltrnl psqelpqeds llhgqfsqav tplahhhtdy skptdiswrđ t1sqkfgssd
181 hlek1fkmdē asaqllayke kghsqssqfs sdqēiahllp envsalpatv avasphttsa
241 tpkpatllpt nasvtpsgts qpqlattapp vttvtsqppt tlistvftra aatlqamatt
301 avlttttfqap tdskslet1 pfteisnlt1 ntgnvynpta lsmsnvesst mnktaswegr
361 easpgsssqg svpenqyglp fekwlligs1 lfgvlflvig lvllgrilse slrrkrysrl
421 dylingiyvd i
//

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Range: from  to 
 Features:
 ☐ SNP
 ☐ CDS
 ☒ NGS
 ☐ HPRD
 ☐ STS

☒ 1: [Q9H8J5](#). Reports MANSC domain cont...[gi:48428493]

[Blink Links](#)

LOCUS Q9H8J5 431 aa linear PRI 01-MAY-2005  
 DEFINITION MANSC domain containing protein 1 precursor (UNQ316/PRO361).  
 ACCESSION Q9H8J5  
 VERSION Q9H8J5 GI:48428493  
 DBSOURCE swissprot: locus MANS1\_HUMAN, accession [Q9H8J5](#);  
 class: standard.  
 extra accessions:Q8NEC1,created: Jul 5, 2004.  
 sequence updated: Jul 5, 2004.  
 annotation updated: May 1, 2005.  
 xrefs: [AK023622.1](#), [BAB14621.1](#), [AY358563.1](#), [AAQ88926.1](#), [BCC32998.2](#),  
[AAH32998.1](#)  
 xrefs (non-sequence databases): EnsemblENSG00000111261,  
 GenewHGNC:25505, InterProIPR011106, PfamPF07502, PROSITEPS50986  
 KEYWORDS Glycoprotein; Polymorphism; Signal; Transmembrane.  
 SOURCE Homo sapiens (human)  
 ORGANISM [Homo sapiens](#)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 REFERENCE 1 (residues 1 to 431)  
 AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R.,  
 Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H.,  
 Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,  
 Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y.,  
 Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M.,  
 Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,  
 Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T.,  
 Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K.,  
 Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H.,  
 Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M.,  
 Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S.,  
 Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A.,  
 Hara,H., Tanase,T.O., Nomura,Y., Togiya,S., Komai,F., Hara,R.,  
 Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A.,  
 Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T.,  
 Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S.,  
 Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H.,  
 Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T.,  
 Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K.,  
 Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M.,  
 Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y.,  
 Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N.,  
 Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T.,  
 Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K.,  
 Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T.,  
 Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J.,  
 Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K.,  
 Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R.,  
 Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.  
 TITLE Complete sequencing and characterization of 21,243 full-length  
 human cDNAs  
 JOURNAL Nat. Genet. 36 (1), 40-45 (2004)  
 PUBMED [14702039](#)  
 REMARK NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].  
 TISSUE=Placenta  
 REFERENCE 2 (residues 1 to 431)  
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,  
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,  
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,  
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,

Lee, J., Lewis, L., Liao, D., Mark, M., Robbie, E., Sanchez, C., Schoenfeld, J., Seshagiri, S., Simmons, L., Singh, J., Smith, V., Stinson, J., Vagts, A., Vandlen, R., Watanabe, C., Wieand, D., Woods, K., Xie, M. H., Yansura, D., Yi, S., Yu, G., Yuan, J., Zhang, M., Zhang, Z., Goddard, A., Wood, W. I., Godowski, P. and Gray, A.

**TITLE** The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment

**JOURNAL** Genome Res. 13 (10), 2265-2270 (2003)

**PUBMED** 12975309

**REMARK** NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

**REFERENCE** 3 (residues 1 to 431)

**AUTHORS** Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Loquellano, N. A., Peters, G. J., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Worley, K. C., Hale, S., Garcia, A. M., Gay, L. J., Hulyk, S. W., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A. C., Shevchenko, Y., Bouffard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butterfield, Y. S., Krzywinski, M. I., Skalska, U., Smailus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.

**CONSRTM** Mammalian Gene Collection Program Team

**TITLE** Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

**PUBMED** 12477932

**REMARK** NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA], AND VARIANT ILE-55. TISSUE=Testis

**COMMENT** [SUBCELLULAR LOCATION] Type I membrane protein (Potential). [SIMILARITY] Contains 1 MANSC domain.

**FEATURES**

**source** Location/Qualifiers

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/organism="Homo sapiens"

/db\_xref="taxon:9606"

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/gene="MANSC1"

**Protein** 1..431

/gene="MANSC1"

/product="MANSC domain containing protein 1 precursor"

**Region** 1..26

/gene="MANSC1"

/region\_name="Signal"

/note="Potential."

/evidence=not\_experimental

**Region** 27..431

/gene="MANSC1"

/region\_name="Mature chain"

/note="MANSC domain containing protein 1."

/evidence=experimental

**Region** 27..385

/gene="MANSC1"

/region\_name="Domain"

/note="Extracellular (Potential)."

/evidence=not\_experimental

**Region** 33..117

/gene="MANSC1"

/region\_name="Domain"

/note="MANSC."

/evidence=experimental

**Region** 55

/gene="MANSC1"

/region\_name="Variant"

/note="V -> I (in dbSNP:3741798). /FTId=VAR\_021840."

/evidence=experimental

**Site** 72

/gene="MANSC1"

/site\_type="glycosylation"

/note="N-linked (GlcNAc...) (Potential)."

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/evidence=not_experimental
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/gene="MANSC1"
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/note="N-linked (GlcNAc...) (Potential)."
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Region 237..332

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/gene="MANSC1"
/region_name="Domain"
/note="Thr-rich."
/evidence=experimental
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Site 327

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Site 352

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Region 375

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Region 386..408

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Region 409..431

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ORIGIN

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121 tdfpsltrnl psqelpqeds llhgqfsqav tplahhhtdy skptdiswrd tlsqkfgssd
181 hleklfkmde asaqllyake khsgqssqfs sdqeahllp envsalpatv avasphttsa
241 tpkpatllpt nasvtpsgts qpqlattapp vttvtsqppt tlistvftra aatlqamatt
301 avlttttfqap tdsqgsletl pftesnltl ntgnvynpta lsmsnvesst mnktaswegr
361 easpgsssqg svpenqyglp fekwlligsf lfgvflfvig lvllgrilse slrrkrysrl
421 dylingiyvd i
```

//

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